GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 18:34:00 ; Search time 5328 Seconds
(without alignments)
10746.274 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcggtctcggagcga.....ctgcgtaggtgaaaaggcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	2.0	50	6	AX199566	AX199566 Sequence
2	24	1.8	30	6	AR242044	AR242044 Sequence
3	24	1.8	50	6	AR232180	AR232180 Sequence
4	23	1.7	25	6	AR028113	AR028113 Sequence
5	23	1.7	25	6	AR030289	AR030289 Sequence
6	23	1.7	25	6	I42108	I42108 Sequence 3
c 7	23	1.7	30	6	I84401	I84401 Sequence 2
c 8	23	1.7	31	6	A01419	A01419 Malaria par
9	23	1.7	33	6	I84406	I84406 Sequence 7
c 10	23	1.7	45	6	AR366218	AR366218 Sequence
c 11	23	1.7	47	6	AX539586	AX539586 Sequence
12	23	1.7	47	6	AX539587	AX539587 Sequence
13	23	1.7	48	6	AR366215	AR366215 Sequence
c 14	23	1.7	48	6	AX539588	AX539588 Sequence
15	23	1.7	48	6	AX539589	AX539589 Sequence
c 16	23	1.7	50	6	AX539582	AX539582 Sequence
17	23	1.7	50	6	AX539583	AX539583 Sequence
c 18	22	1.7	22	6	AR336835	AR336835 Sequence
c 19	22	1.7	38	6	AX539590	AX539590 Sequence
20	22	1.7	38	6	AX539591	AX539591 Sequence
c 21	22	1.7	39	6	AX539592	AX539592 Sequence
22	22	1.7	39	6	AX539593	AX539593 Sequence
c 23	21	1.6	21	6	AR084563	AR084563 Sequence
c 24	21	1.6	21	6	AR084566	AR084566 Sequence
25	21	1.6	21	6	AR084567	AR084567 Sequence
c 26	21	1.6	21	6	AR084578	AR084578 Sequence
27	21	1.6	21	6	AR084579	AR084579 Sequence
28	21	1.6	21	6	AR084582	AR084582 Sequence
29	21	1.6	21	6	AR093142	AR093142 Sequence
c 30	21	1.6	39	6	E50506	E50506 Method for
31	21	1.6	39	6	E50507	E50507 Method for
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34	20	1.5	20	6	AR182885	AR182885 Sequence
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37	20	1.5	20	6	AX355382	AX355382 Sequence
38	20	1.5	20	6	AX547104	AX547104 Sequence
39	20	1.5	20	6	BD069976	BD069976 Use of nu
c 40	20	1.5	24	6	AR078306	AR078306 Sequence
41	20	1.5	24	6	AR078307	AR078307 Sequence
42	20	1.5	28	6	AX034217	AX034217 Sequence
c 43	20	1.5	50	6	A62658	A62658 Sequence 22
c 44	20	1.5	50	6	AR144730	AR144730 Sequence
45	20	1.5	50	6	AR232179	AR232179 Sequence

ALIGNMENTS

RESULT 1
AX199566
LOCUS AX199566 50 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 496 from Patent WO0151670.
ACCESSION AX199566
VERSION AX199566.1 GI:15389997
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

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  JOURNAL   Patent: WO 0151670-A 496 19-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg42747251"
     misc_feature    26
                     /note="2 of 2 allelic variants (495 is other entry)"
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Qy        618 CACGGTCCTTCATCAGCCGGCACAGC 643
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Db          1 CACGGTCCTTCATCAGCCGGCACAGC 26


RESULT 2
AR242044
LOCUS       AR242044                  30 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 332 from patent US 6472154.
ACCESSION   AR242044
VERSION     AR242044.1  GI:27287856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 332 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
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ORIGIN

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Qy         56 GGCGGCGGCGGCGGCGGCGGCGGA 79
              ||||||||||||||||||||||||
Db          7 GGCGGCGGCGGCGGCGGCGGCGGA 30


RESULT 3
AR232180
LOCUS       AR232180                  50 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 14 from patent US 6455292.
ACCESSION   AR232180
VERSION     AR232180.1  GI:27274071
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shu,Y., Fan,W., Kovacs,K.F., Zidanic,M. and Jay,G.
  TITLE     Full-length serine protein kinase in brain and pancreas
  JOURNAL   Patent: US 6455292-A 14 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .50
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGGA 79
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Db         23 GGCGGCGGCGGCGGCGGCGGCGGA 46


RESULT 4
AR028113
LOCUS       AR028113                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5858649.
ACCESSION   AR028113
VERSION     AR028113.1  GI:5940086
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Asgari,M., Blick,M., Bresser,J., Cubbage,M.Lee. and Prashad,N.
  TITLE     Amplification of mRNA for distinguishing fetal cells in maternal
            blood
  JOURNAL   Patent: US 5858649-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .25
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             1.7%;  Score 23;  DB 6;  Length 25;
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 5
AR030289
LOCUS       AR030289                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5861253.
ACCESSION   AR030289
VERSION     AR030289.1  GI:5943503
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Asgari,M., Blick,M., Bresser,J., Cubbage,M.Lee. and Prashad,N.
  TITLE     Intracellular antigens for identifying fetal cells in maternal
            blood
  JOURNAL   Patent: US 5861253-A 3 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .25
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ORIGIN

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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 6
I42108
LOCUS       I42108                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5629147.
ACCESSION   I42108
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VERSION     I42108.1  GI:2467603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Asgari,M., Blick,M., Bresser,J., Cubbage,M.L. and Prashad,N.
  TITLE     Enriching and identifying fetal cells in maternal blood for in situ
            hybridization
  JOURNAL   Patent: US 5629147-A 3 13-MAY-1997;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 7
I84401/c
LOCUS       I84401                    30 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 2 from patent US 5695933.
ACCESSION   I84401
VERSION     I84401.1  GI:3021921
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Schalling,M., Hudson,T.J. and Housman,D.E.
  TITLE     Direct detection of expanded nucleotide repeats in the human genome
  JOURNAL   Patent: US 5695933-A 2 09-DEC-1997;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db         29 GGCGGCGGCGGCGGCGGCGGCGG 7


RESULT 8
A01419/c
LOCUS       A01419                    31 bp    DNA     linear   PAT 28-APR-1993
DEFINITION  Malaria parasitic epitope (T-cell).
ACCESSION   A01419
VERSION     A01419.1  GI:344347
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   .
  JOURNAL   Patent: WO 8810300-A 23 29-DEC-1988;
FEATURES             Location/Qualifiers
     source          1. .31
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             1.7%;  Score 23;  DB 6;  Length 31;
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db         30 GGCGGCGGCGGCGGCGGCGGCGG 8


RESULT 9
I84406
LOCUS       I84406                    33 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 7 from patent US 5695933.
ACCESSION   I84406
VERSION     I84406.1  GI:3021926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Schalling,M., Hudson,T.J. and Housman,D.E.
  TITLE     Direct detection of expanded nucleotide repeats in the human genome
  JOURNAL   Patent: US 5695933-A 7 09-DEC-1997;
FEATURES             Location/Qualifiers
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 10
AR366218/c
LOCUS       AR366218                  45 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 22 from patent US 6329147.
ACCESSION   AR366218
VERSION     AR366218.1  GI:34598600
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Wagner,R.E. Jr.
  TITLE     Methods for detection of a triplet repeat block and a functional
            mismatch binding protein in a biological fluid sample
  JOURNAL   Patent: US 6329147-A 22 11-DEC-2001;
FEATURES             Location/Qualifiers
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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RESULT 11
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LOCUS       AX539586                  47 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 373 from Patent WO02059142.
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ACCESSION   AX539586
VERSION     AX539586.1  GI:25273135
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 373 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db         37 GGCGGCGGCGGCGGCGGCGGCGG 15


RESULT 12
AX539587
LOCUS       AX539587                 47 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 374 from Patent WO02059142.
ACCESSION   AX539587
VERSION     AX539587.1  GI:25273137
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 374 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
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Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
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Db         11 GGCGGCGGCGGCGGCGGCGGCGG 33


RESULT 13
AR366215
LOCUS       AR366215                 48 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 19 from patent US 6329147.
ACCESSION   AR366215
VERSION     AR366215.1  GI:34598597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Wagner,R.E. Jr.
  TITLE     Methods for detection of a triplet repeat block and a functional
            mismatch binding protein in a biological fluid sample
  JOURNAL   Patent: US 6329147-A 19 11-DEC-2001;
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     source          1. .48
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RESULT 14
AX539588/c
LOCUS       AX539588                 48 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 375 from Patent WO02059142.
ACCESSION   AX539588
VERSION     AX539588.1  GI:25273139
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 375 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
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RESULT 15
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DEFINITION  Sequence 376 from Patent WO02059142.
ACCESSION   AX539589
VERSION     AX539589.1  GI:25273140
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 376 01-AUG-2002;
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Job time : 5330 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 18:02:49 ; Search time 580 Seconds
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9675.637 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcggtctcggagcga.....ctgcgtaggtgaaaaggcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3185356

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	26	2.0	50	4	AAH89715	Aah89715 Human cod
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	3	24	1.8	30	7	ABX80007	Abx80007 EST polym
	4	24	1.8	50	7	ABX13592	Abx13592 Human ser
	5	24	1.8	50	9	AAD60995	Aad60995 Human ser
	6	23	1.7	25	2	AAQ55856	Aaq55856 Fragile X
	7	23	1.7	25	2	AAQ85271	Aaq85271 Probe for
	8	23	1.7	25	2	AAX05267	Aax05267 Fragile X
c	9	23	1.7	45	3	AAC60682	Aac60682 Triplet r
c	10	23	1.7	45	6	AAD40340	Aad40340 Test DNA
	11	23	1.7	47	6	ABS67036	Abs67036 Human MRP
c	12	23	1.7	47	6	ABS67035	Abs67035 Human MRP
	13	23	1.7	48	3	AAC60679	Aac60679 Triplet r
	14	23	1.7	48	6	AAD40337	Aad40337 Test DNA
c	15	23	1.7	48	6	ABS67037	Abs67037 Human MRP
	16	23	1.7	48	6	ABS67038	Abs67038 Human MRP
c	17	23	1.7	50	6	ABS67031	Abs67031 Human MRP
	18	23	1.7	50	6	ABS67032	Abs67032 Human MRP
c	19	23	1.7	50	7	ABZ22157	Abz22157 E. coli i
c	20	22	1.7	22	9	AAD60109	Aad60109 Human PME
	21	22	1.7	38	6	ABS67040	Abs67040 Human MRP
c	22	22	1.7	38	6	ABS67039	Abs67039 Human MRP
	23	22	1.7	39	6	ABS67042	Abs67042 Human MRP
c	24	22	1.7	39	6	ABS67041	Abs67041 Human MRP
c	25	22	1.7	41	6	ABZ47846	Abz47846 Human ATP
	26	22	1.7	41	6	AAK99304	Aak99304 Human can
	27	22	1.7	41	6	AAK99303	Aak99303 Human can
	28	21	1.6	21	3	AAZ44349	Aaz44349 Protein k
c	29	21	1.6	21	6	ABK99279	Abk99279 Hepatitis
c	30	21	1.6	21	9	ADC16572	Adc16572 Short int
	31	21	1.6	21	9	ADC16571	Adc16571 Short int
c	32	21	1.6	39	4	AAH27630	Aah27630 Upper str
	33	21	1.6	39	4	AAH27631	Aah27631 Lower str
	34	20	1.5	20	2	AAV47686	Aav47686 Unmethyla
	35	20	1.5	20	2	AAV74243	Aav74243 CpG-N mot
	36	20	1.5	20	4	AAF99116	Aaf99116 Immunosti
	37	20	1.5	20	6	ABS77759	Abs77759 Angiogene
	38	20	1.5	20	6	ABL39008	Abl39008 Immunosti
	39	20	1.5	20	8	ACD99549	Acd99549 Immunosti
	40	20	1.5	20	8	ADB36618	Adb36618 Immunosti
	41	20	1.5	20	9	AAD60110	Aad60110 Human PME
	42	20	1.5	24	2	AAZ24999	Aaz24999 Sense pro
c	43	20	1.5	24	2	AAZ24998	Aaz24998 Antisense
	44	20	1.5	28	3	AAA64342	Aaa64342 Forward P
	45	20	1.5	33	2	AAQ73441	Aaq73441 Crohn's d

ALIGNMENTS

RESULT 1
AAH89715
ID AAH89715 standard; DNA; 50 BP.
XX
AC AAH89715;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 496.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000322.
XX
PR 07-JAN-2000; 2000US-0174962P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
DR P-PSDB; AAM00598.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX
PS Claim 1; Page 246; 475pp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing

```
CC   oligonucleotide fragment of the invention
XX
SQ   Sequence 50 BP; 12 A; 15 C; 18 G; 5 T; 0 U; 0 Other;

  Query Match             2.0%;  Score 26;  DB 4;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        618 CACGGTCCTTCATCAGCCGGCACAGC 643
              ||||||||||||||||||||||||||
Db          1 CACGGTCCTTCATCAGCCGGCACAGC 26


RESULT 2
ABZ84399/c
ID   ABZ84399 standard; DNA; 25 BP.
XX
AC   ABZ84399;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant human PCR primer #1558.
XX
KW   Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 346; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 25 BP; 4 A; 6 C; 9 G; 6 T; 0 U; 0 Other;

  Query Match             1.9%;  Score 25;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1105 CTACAGCGAGGTCATCGGCCACTAC 1129
              |||||||||||||||||||||||||
Db         25 CTACAGCGAGGTCATCGGCCACTAC 1


RESULT 3
ABX80007
ID   ABX80007 standard; cDNA; 30 BP.
XX
AC   ABX80007;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #332.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 1163; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 30 BP; 1 A; 9 C; 20 G; 0 T; 0 U; 0 Other;

  Query Match             1.8%;  Score 24;  DB 7;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          56 GGCGGCGGCGGCGGCGGCGGCGGA 79
               ||||||||||||||||||||||||
Db           7 GGCGGCGGCGGCGGCGGCGGCGGA 30
```

RESULT 4
ABX13592
ID ABX13592 standard; DNA; 50 BP.
XX
AC ABX13592;
XX
DT 10-FEB-2003 (first entry)
XX
DE Human serine protein kinase KSE336 promoter fragment #8.
XX
KW Human; promoter; ds; chromosome 11p15.5-pter; astrocytoma; meningioma;
KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
KW helicoid peripapillary chorioretinal degeneration; brain; pancreas;
KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
XX
OS Homo sapiens.
XX
PN US6455292-B1.
XX
PD 24-SEP-2002.
XX
PF 16-AUG-2001; 2001US-00930181.
XX
PR 16-AUG-2001; 2001US-00930181.
XX
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;
XX
DR WPI; 2003-066233/06.
XX
PT New isolated polynucleotide coding without interruption for a human
PT KSE336 polypeptide useful for preventing or treating diseases/conditions
PT relating to brain and pancreas, e.g. meningioma, insulin-dependent
PT diabetes mellitus 2.
XX
PS Disclosure; Col 55; 34pp; English.
XX
CC The invention relates to an isolated polynucleotide (its complement or a
CC sequence 99% similar to it) coding without interruption for a human
CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
CC included is a method of identifying an agent that modulates the
CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
CC progenitor cells comprising: (a) contacting a cell population comprising
CC the cells with a test agent under conditions effective for the test agent
CC to modulate the expression of KSE336; and (b) determining if the test
CC agent modulates the expression of KSE336. The polynucleotides are useful
CC as molecular targets or drug targets, and for detecting, diagnosing,
CC staging, monitoring, prognosticating, preventing or treating diseases or
CC conditions relating to brain and pancreas, such as astrocytoma,
CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
CC mellitus 2, helicoid peripapillary chorioretinal degeneration, Beckwith-
CC Wiedemann syndrome or congenital hyperinsulinism. The method and
CC polynucleotides are useful in research, diagnosis, drug discovery,
CC therapy, clinical medicine, forensic science and pathology. The gene for
CC KSE336 is located on chromosome 11p15.5-pter. The present sequence is
CC promoter fragment of the KSE366 gene
XX
SQ Sequence 50 BP; 2 A; 17 C; 30 G; 1 T; 0 U; 0 Other;

```
  Query Match             1.8%;  Score 24;  DB 7;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          56 GGCGGCGGCGGCGGCGGCGGCGGA 79
               ||||||||||||||||||||||||
Db          23 GGCGGCGGCGGCGGCGGCGGCGGA 46
```

RESULT 5
AAD60995
ID AAD60995 standard; DNA; 50 BP.
XX
AC AAD60995;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human serine/threonine kinase KSE336 promoter DNA #8.
XX
KW Human; KSE336 protein; serine/threonine kinase; STK; pancreas disease;
KW brain disease; astrocytoma; meningioma; pancreatic adenocarcinoma;
KW insulin-dependent diabetes mellitus; Beckwith-Wiedemann syndrome;
KW congenital hyperinsulinism; immunotherapy; immunosuppressive; cytostatic;
KW ds.
XX
OS Homo sapiens.
XX
PN US2003092036-A1.
XX
PD 15-MAY-2003.
XX
PF 15-JUL-2002; 2002US-00195072.
XX
PR 16-AUG-2001; 2001US-00930181.
XX
PA (SHUY/) SHU Y.
PA (FANW/) FAN W.
PA (KOVA/) KOVACS K F.
PA (ZIDA/) ZIDANIC M.
PA (JAYG/) JAY G.
XX
PI Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;
XX
DR WPI; 2003-765475/72.
XX
PT New isolated KSE336 polynucleotide useful for treating meningioma
PT pancreatic adenocarcinoma, helicoid peripapillary chorioretinal
PT degeneration, insulin-dependent diabetes mellitus 2, and congenital
PT hyperinsulinism.
XX
PS Disclosure; Page 19; 0pp; English.
XX
CC The present invention relates to KSE336 polynucleotides encoding serine/
CC threonine kinase (STK) proteins. Sequences of the invention are useful
CC for diagnosing a brain or pancreas disease associated with abnormal
CC KSE336, or susceptibility to the disease. They are useful for assessing a
CC therapeutic or preventative intervention in a subject having a brain or
CC pancreas disease. The invention is useful for identifying an agent that
CC modulates the expression of KSE336 in brain or pancreas cells, cells
CC derived from brain and pancreas or brain and pancreas progenitor cells.
CC It is useful for detecting polymorphisms in KSE336. It is also useful for
CC advertising KSE336 for sale, commercial use or licensing. KSE336
CC sequences are useful to treat diseases such as astrocytoma, meningioma,
CC pancreatic adenocarcinoma, insulin-dependent diabetes mellitus, Beckwith-
CC Wiedemann syndrome or congenital hyperinsulinism. They are also useful in
CC immunotherapy. The present sequence is human KSE336 promoter DNA
XX
SQ Sequence 50 BP; 2 A; 17 C; 30 G; 1 T; 0 U; 0 Other;

```
  Query Match             1.8%;  Score 24;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          56 GGCGGCGGCGGCGGCGGCGGCGGA 79
               ||||||||||||||||||||||||
Db          23 GGCGGCGGCGGCGGCGGCGGCGGA 46
```

RESULT 6
AAQ55856

ID AAQ55856 standard; DNA; 25 BP.
XX
AC AAQ55856;
XX
DT 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
DE Fragile X probe.
XX
KW FC; foetal cells; marker; probe; hybridise; denature; dye; label;
KW fluroescent; kit; detection; haemoglobin; rhesus; gamma globulin; NR;
KW nitrogen reductase; ss.
XX
OS Homo sapiens.
XX
PN WO9402646-A1.
XX
PD 03-FEB-1994.
XX
PF 19-JUL-1993; 93WO-US006828.
XX
PR 17-JUL-1992; 92US-00915965.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Asgari M, Prashad N, Cubbage ML, Ju S, Blick M, Bresser J;
XX
DR WPI; 1994-048903/06.
XX
PT Identifying foetal cells, conc. from maternal blood, using specific
PT marker - e.g. surface antigen, before in situ hybridisation of target
PT nucleic acid to detect viral infection, genetic abnormality, etc.
XX
PS Disclosure; Page 73; 109pp; English.
XX
CC Probes (AAQ55857-873) detect regions of 3 fragments of the HUMGLBN gene
CC (AAQ64058). Bases 1-91 correspond to bases 2179-2269 of HUMGLBN, bases 92
CC -314 are from 2393-2615 of HUMGLBN and bases 315-443 are from 3502-3630
CC of HUMGLBN. The probes (AAQ55854-55) were used as control, positive and
CC negative genetic testing probes. Probe (AAQ55856) was used to detect the
CC fragile X condition (Example 14) (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 1.7%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 2 GGCGGCGGCGGCGGCGGCGGCGG 24

RESULT 7
AAQ85271
ID AAQ85271 standard; DNA; 25 BP.
XX
AC AAQ85271;
XX
DT 25-MAR-2003 (revised)
DT 24-AUG-1995 (first entry)
XX
DE Probe for Fragile X condition.
XX
KW Prenatal diagnosis; fragile X; probe; ss.
XX
OS Synthetic.
XX
PN WO9503431-A1.
XX
PD 02-FEB-1995.
XX
PF 19-JUL-1994; 94WO-US008342.
XX
PR 19-JUL-1993; 93US-00094710.
XX
PA (APRO-) APROGENEX INC.
XX
PI Bresser J, Weber WD, Ryusaki T, Prashad N, Cubbage ML, Blick M;
PI Asgari M, Poindexter BJ;
XX
DR WPI; 1995-075255/10.
XX
PT Identifying foetal cells in samples contg. maternal cells - used for
PT monitoring foetus status, identifying sex or detecting genetic
PT abnormalities or viral infection.
XX
PS Example; Page 75; 115pp; English.
XX
CC In the example, Fragile X Chromosome is identified in amniocytes and in
CC peripheral blood mononuclear cells. The 5' aminohexyl oligos is coupled
CC to the fluorescent dye fluroescein. When an amplification of the CGG DNA
CC fragment (of the X chromosome in Xq27.3) is present, there is an increase
CC in the intensity of the signal. (Updated on 25-MAR-2003 to correct PN
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 1.7%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 2 GGCGGCGGCGGCGGCGGCGGCGG 24

RESULT 8
AAX05267
ID AAX05267 standard; DNA; 25 BP.
XX
AC AAX05267;
XX
DT 14-APR-1999 (first entry)
XX
DE Fragile X chromosome detecting probe.
XX
KW Genetic testing; foetal cell; maternal; blood; pregnant; hybridisation;
KW detection; HIV, hepatitis virus; herpes virus; chromosomal abnormality;
KW probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5858649-A.
XX
PD 12-JAN-1999.
XX
PF 31-DEC-1996; 96US-00775609.
XX
PR 17-JUL-1992; 92US-00915765.
PR 19-JUL-1993; 93US-00094710.
PR 19-JUL-1994; 94WO-US008342.
PR 17-JAN-1995; 95US-00374144.
XX
PA (APRO-) APROGENEX INC.
XX
PI Blick M, Cubbage ML, Bresser J, Prashad N, Asgari M;
XX
DR WPI; 1999-152096/13.
XX
PT Method for distinguishing foetal cells from adult cells in blood - based
PT on amplification and detection of mRNA selectively expressed in foetal
PT cells.
XX

PS Example 4, 14; Col 49; 49pp; English.
XX
CC The invention relates to a method of enriching foetal cells from maternal
CC blood and for identifying such foetal cells. Foetal cells can be
CC distinguished from adult cells in a blood specimen by (a) treating a
CC blood specimen from a pregnant female to yield a mixture of cells
CC comprising foetal cells and adult cells; (b) amplifying one or more mRNAs
CC within the cells, the mRNAs being selectively expressed in target foetal
CC cells to be distinguished but not expressed in adult blood cells; (c)
CC performing in situ hybridisation on the cells under hybridising
CC conditions suitable to maintain cell membranes in a substantially intact
CC state and with a hybridisation medium comprising a detectably labelled
CC probe complementary to the amplified mRNA that is selectively expressed
CC in the target foetal cells but not expressed in adult blood cells; (d)
CC removing the hybridisation medium and unhybridised probe from the mixture
CC of cells to yield hybridised cells, and (e) detecting the labelled probe
CC remaining in the hybridised cells; whereby cells in which the labelled
CC probe is detected are identified as the target foetal cells; A second
CC method for determining the presence of a target nucleotide sequence in
CC individual foetal cells present in a cellular specimen is also provided.
CC The methods (especially the second) is useful for detecting HIV,
CC hepatitis viruses or herpes viruses in foetal cells, or for detecting
CC chromosomal abnormalities in foetal cells. The present sequence
CC represents a probe used for the detection of the Fragile X chromosome in
CC amniocytes and in peripheral blood mononuclear cells
XX
SQ Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 1.7%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 2 GGCGGCGGCGGCGGCGGCGGCGG 24

RESULT 9
AAC60682/c
ID AAC60682 standard; DNA; 45 BP.
XX
AC AAC60682;
XX
DT 29-JAN-2001 (first entry)
XX
DE Triplet repeat block exemplary test sequence #3.
XX
KW Mismatch-binding protein; MutS; hexA; MBP; hMSH2; forensic medicine;
KW disease diagnosis; cancer; epidemiology; allele identification;
KW infectious agent; triplet repeat; PCR primer; probe; ss.
XX
OS Unidentified.
XX
PN US6120992-A.
XX
PD 19-SEP-2000.
XX
PF 04-MAR-1996; 96US-00608016.
XX
PR 04-NOV-1993; 93US-00147785.
PR 28-APR-1995; 95US-00431081.
XX
PA (VALI-) VALIGENE CORP.
XX
PI Wagner RE;
XX
DR WPI; 2000-601481/57.
XX
PT Use of immobilized MutS protein that binds to nucleic acid hybrid with
PT single base mismatch, for detecting in test DNA sample from diseased
PT human, presence of heteroduplex having deletion or addition 4
PT nucleotides.
XX
PS Disclosure; Fig 12a; 62pp; English.
XX
CC The present invention is concerned with the detection of DNA sequences
CC which may have a single mismatched base or up to 4 bases inserted or
CC deleted from the sequence when compared with the wild-type. The E. coli
CC MutS protein or its homologues (for example hexA and hMSH2) can be used
CC to bind to a sample containing the nucleic acid sequence of interest and
CC a wild-type sequence. If there is a mismatch, the MutS protein will bind
CC to the duplex and can then be detected. This method can be used in the
CC diagnosis of diseases such as cancer and those caused by triplet repeat
CC expansions, including Fragile X syndrome, myotonic dystrophy,
CC Huntington's disease, spino-cerebellar ataxia type 1, spinal bulbar
CC muscular atrophy, Machado-Joseph disease and dentatorubralpallidoluysian
CC atrophy. It can also be used to detect and determine the epidemiology of
CC infectious diseases, in specific allele identification and to detect
CC mutations and polymorphisms. The sequences shown in AAC60661-C60683 were
CC all used to demonstrate the method
XX
SQ Sequence 45 BP; 0 A; 18 C; 9 G; 0 T; 0 U; 18 Other;

Query Match 1.7%; Score 23; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 35 GGCGGCGGCGGCGGCGGCGGCGG 13

RESULT 10
AAD40340/c
ID AAD40340 standard; DNA; 45 BP.
XX
AC AAD40340;
XX
DT 22-OCT-2002 (first entry)
XX
DE Test DNA #3 used in the triplet repeat diagnostic method.
XX
KW Mismatch binding protein; heteroduplex DNA; triplet repeat block; TRB;
KW fragile X syndrome; myotonic dystrophy; Huntington's disease;
KW spino-cerebellar ataxia type I; spinal bulbar muscular atrophy;
KW Machado-Joseph disease; dentatorubralpallidoluysian atrophy; ss.
XX
OS Unidentified.
XX
PN US6329147-B1.
XX
PD 11-DEC-2001.
XX
PF 04-FEB-2000; 2000US-00497933.
XX
PR 04-NOV-1993; 93US-00147785.
PR 28-APR-1995; 95US-00431081.
PR 04-MAR-1996; 96US-00608016.
XX
PA (VALI-) VALIGEN US INC.
XX
PI Wagner RE;
XX
DR WPI; 2002-187350/24.
XX
PT Determining mismatch binding protein in sample comprises mixing sample
PT with labeled heteroduplex DNA, contacting mixture with immobilized
PT mismatch binding protein and detecting amount of DNA bound and comparing
PT with control.
XX
PS Disclosure; Fig 12B; 62pp; English.
XX
CC The invention relates to a method for determining the presence of a
CC functional mismatch binding protein. The method comprising mixing
CC biological fluid sample with detectably labelled heteroduplex DNA to form
CC a mixture, contacting the mixture with immobilised mismatch-binding

```
CC   protein, detecting the binding of the DNA to the protein and comparing
CC   the amount of the heteroduplex DNA bound with the amount of the DNA bound
CC   when control sample is utilised instead of fluid sample. The method is
CC   useful for determining the presence of a functional mismatch-binding
CC   protein in a biological fluid sample preferably presence of a repeat
CC   block especially a triplet repeat block (TRB) of unit sequence 5'-(CGG)_n
CC   or 5'-(CTG)_n 3'-(GCC)_n 3'-(GAC)_n in test DNA in a sample preferably by
CC   a competitive assay method, where TRB is longer (or shorter) than TRB in
CC   a diagnostic oligonucleotide probe, and n is an integer and is number of
CC   repeats of TRB in the test DNA. The method is useful for diagnosing a
CC   variety of disease states or susceptibilities such as fragile X syndrome,
CC   myotonic dystrophy, Huntington's disease, spino-cerebellar ataxia type I,
CC   spinal bulbar muscular atrophy, Machado-Joseph disease and
CC   dentatorubralpallidoluysian atrophy. The present sequence is test DNA
CC   used in the triplet repeat diagnostic method
XX
SQ   Sequence 45 BP; 0 A; 18 C; 9 G; 0 T; 0 U; 18 Other;

  Query Match              1.7%;  Score 23;  DB 6;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db         35 GGCGGCGGCGGCGGCGGCGGCGG 13


RESULT 11
ABS67036
ID   ABS67036 standard; DNA; 47 BP.
XX
AC   ABS67036;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human MRP-1 polymorphic DNA region #298.
XX
KW   Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW   renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200259142-A2.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-EP000796.
XX
PR   26-JAN-2001; 2001EP-00101651.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI   Brinkmann U,  Hoffmeyer S,  Mornhinweg E;
XX
DR   WPI; 2002-657475/70.
XX
PT   Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT   diagnosis and treatment of cancer and multidrug resistance related
PT   diseases, and for identifying single nucleotide polymorphisms.
XX
PS   Claim 1; Page 85; 198pp; English.
XX
CC   The invention relates to a multidrug resistance-associated protein 1 (MRP
CC   -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC   for identifying a single nucleotide polymorphism and for identifying and
CC   obtaining a pro-drug or drug capable of modulating the activity of a
CC   molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC   of the activity of a molecular variant of MRP-1. The sequences are useful
CC   for diagnosing a disorder related to the presence of a molecular variant
CC   of MRP-1 or susceptibility to such a disorder, where the disorder is
CC   cancer (particularly renal cancer) or a disease related to multidrug
CC   resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ   Sequence 47 BP; 3 A; 15 C; 27 G; 2 T; 0 U; 0 Other;

  Query Match              1.7%;  Score 23;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db         11 GGCGGCGGCGGCGGCGGCGGCGG 33


RESULT 12
ABS67035/c
ID   ABS67035 standard; DNA; 47 BP.
XX
AC   ABS67035;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human MRP-1 polymorphic DNA region #297.
XX
KW   Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW   renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200259142-A2.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-EP000796.
XX
PR   26-JAN-2001; 2001EP-00101651.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI   Brinkmann U,  Hoffmeyer S,  Mornhinweg E;
XX
DR   WPI; 2002-657475/70.
XX
PT   Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT   diagnosis and treatment of cancer and multidrug resistance related
PT   diseases, and for identifying single nucleotide polymorphisms.
XX
PS   Claim 1; Page 85; 198pp; English.
XX
CC   The invention relates to a multidrug resistance-associated protein 1 (MRP
CC   -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC   for identifying a single nucleotide polymorphism and for identifying and
CC   obtaining a pro-drug or drug capable of modulating the activity of a
CC   molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC   of the activity of a molecular variant of MRP-1. The sequences are useful
CC   for diagnosing a disorder related to the presence of a molecular variant
CC   of MRP-1 or susceptibility to such a disorder, where the disorder is
CC   cancer (particularly renal cancer) or a disease related to multidrug
CC   resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ   Sequence 47 BP; 2 A; 27 C; 15 G; 3 T; 0 U; 0 Other;

  Query Match              1.7%;  Score 23;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db         37 GGCGGCGGCGGCGGCGGCGGCGG 15


RESULT 13
AAC60679
ID   AAC60679 standard; DNA; 48 BP.
XX
AC   AAC60679;
```

XX
DT 29-JAN-2001 (first entry)
XX
DE Triplet repeat block exemplary test sequence #1.
XX
KW Mismatch-binding protein; MutS; hexA; MBP; hMSH2; forensic medicine;
KW disease diagnosis; cancer; epidemiology; allele identification;
KW infectious agent; triplet repeat; PCR primer; probe; ss.
XX
OS Unidentified.
XX
PN US6120992-A.
XX
PD 19-SEP-2000.
XX
PF 04-MAR-1996; 96US-00608016.
XX
PR 04-NOV-1993; 93US-00147785.
PR 28-APR-1995; 95US-00431081.
XX
PA (VALI-) VALIGENE CORP.
XX
PI Wagner RE;
XX
DR WPI; 2000-601481/57.
XX
PT Use of immobilized MutS protein that binds to nucleic acid hybrid with
PT single base mismatch, for detecting in test DNA sample from diseased
PT human, presence of heteroduplex having deletion or addition 4
PT nucleotides.
XX
PS Disclosure; Fig 12a; 62pp; English.
XX
CC The present invention is concerned with the detection of DNA sequences
CC which may have a single mismatched base or up to 4 bases inserted or
CC deleted from the sequence when compared with the wild-type. The E. coli
CC MutS protein or its homologues (for example hexA and hMSH2) can be used
CC to bind to a sample containing the nucleic acid sequence of interest and
CC a wild-type sequence. If there is a mismatch, the MutS protein will bind
CC to the duplex and can then be detected. This method can be used in the
CC diagnosis of diseases such as cancer and those caused by triplet repeat
CC expansions, including Fragile X syndrome, myotonic dystrophy,
CC Huntington's disease, spino-cerebellar ataxia type 1, spinal bulbar
CC muscular atrophy, Machado-Joseph disease and dentatorubralpallidoluysian
CC atrophy. It can also be used to detect and determine the epidemiology of
CC infectious diseases, in specific allele identification and to detect
CC mutations and polymorphisms. The sequences shown in AAC60661-C60683 were
CC all used to demonstrate the method
XX
SQ Sequence 48 BP; 0 A; 10 C; 20 G; 0 T; 0 U; 18 Other;

Query Match 1.7%; Score 23; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 10 GGCGGCGGCGGCGGCGGCGGCGG 32

RESULT 14
AAD40337
ID AAD40337 standard; DNA; 48 BP.
XX
AC AAD40337;
XX
DT 22-OCT-2002 (first entry)
XX
DE Test DNA #1 used in the triplet repeat diagnostic method.
XX
KW Mismatch binding protein; heteroduplex DNA; triplet repeat block; TRB;
KW fragile X syndrome; myotonic dystrophy; Huntington's disease;
KW spino-cerebellar ataxia type I; spinal bulbar muscular atrophy;
KW Machado-Joseph disease; dentatorubralpallidoluysian atrophy; ss.
XX
OS Unidentified.
XX
PN US6329147-B1.
XX
PD 11-DEC-2001.
XX
PF 04-FEB-2000; 2000US-00497933.
XX
PR 04-NOV-1993; 93US-00147785.
PR 28-APR-1995; 95US-00431081.
PR 04-MAR-1996; 96US-00608016.
XX
PA (VALI-) VALIGEN US INC.
XX
PI Wagner RE;
XX
DR WPI; 2002-187350/24.
XX
PT Determining mismatch binding protein in sample comprises mixing sample
PT with labeled heteroduplex DNA, contacting mixture with immobilized
PT mismatch binding protein and detecting amount of DNA bound and comparing
PT with control.
XX
PS Disclosure; Fig 12A; 62pp; English.
XX
CC The invention relates to a method for determining the presence of a
CC functional mismatch binding protein. The method comprising mixing
CC biological fluid sample with detectably labelled heteroduplex DNA to form
CC a mixture, contacting the mixture with immobilised mismatch-binding
CC protein, detecting the binding of the DNA to the protein and comparing
CC the amount of the heteroduplex DNA bound with the amount of the DNA bound
CC when control sample is utilised instead of fluid sample. The method is
CC useful for determining the presence of a functional mismatch-binding
CC protein in a biological fluid sample preferably presence of a repeat
CC block especially a triplet repeat block (TRB) of unit sequence 5'-(CGG)_n
CC or 5'-(CTG)_n 3'-(GCC)_n 3'-(GAC)_n in test DNA in a sample preferably by
CC a competitive assay method, where TRB is longer (or shorter) than TRB in
CC a diagnostic oligonucleotide probe, and n is an integer and is number of
CC repeats of TRB in the test DNA. The method is useful for diagnosing a
CC variety of disease states or susceptibilities such as fragile X syndrome,
CC myotonic dystrophy, Huntington's disease, spino-cerebellar ataxia type I,
CC spinal bulbar muscular atrophy, Machado-Joseph disease and
CC dentatorubralpallidoluysian atrophy. The present sequence is test DNA
CC used in the triplet repeat diagnostic method
XX
SQ Sequence 48 BP; 0 A; 10 C; 20 G; 0 T; 0 U; 18 Other;

Query Match 1.7%; Score 23; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 11 GGCGGCGGCGGCGGCGGCGGCGG 33

RESULT 15
ABS67037/c
ID ABS67037 standard; DNA; 48 BP.
XX
AC ABS67037;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #299.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX

PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 9; Page 85; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 48 BP; 2 A; 27 C; 15 G; 3 T; 0 U; 1 Other;

Query Match 1.7%; Score 23; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
||||||||||||||||||||||||
Db 37 GGCGGCGGCGGCGGCGGCGGCGG 15

Search completed: July 1, 2004, 19:19:07
Job time : 582 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 20:48:10 ; Search time 644 Seconds
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Perfect score: 1321
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3163042 seqs, 2412103800 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726952

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	1.8	50	15	US-10-195-072-14	Sequence 14, Appl
	2	24	1.8	50	15	US-10-195-071-14	Sequence 14, Appl
c	3	23	1.7	23	17	US-10-434-479-78	Sequence 78, Appl
c	4	23	1.7	50	15	US-10-126-448-2	Sequence 2, Appli
c	5	22	1.7	22	15	US-10-390-045-8	Sequence 8, Appli
c	6	22	1.7	22	17	US-10-434-479-8	Sequence 8, Appli
c	7	22	1.7	22	17	US-10-434-479-70	Sequence 70, Appl
c	8	21	1.6	21	9	US-09-828-034-10	Sequence 10, Appl
c	9	21	1.6	39	15	US-10-157-382-7	Sequence 7, Appli
	10	21	1.6	39	15	US-10-157-382-8	Sequence 8, Appli
	11	20	1.5	20	10	US-09-888-326-410	Sequence 410, App
	12	20	1.5	20	10	US-09-776-479-243	Sequence 243, App
	13	20	1.5	20	13	US-10-314-578-243	Sequence 243, App
	14	20	1.5	20	13	US-09-776-479-243	Sequence 243, App
	15	20	1.5	20	15	US-10-112-653-235	Sequence 235, App
	16	20	1.5	20	15	US-10-017-995-243	Sequence 243, App
	17	20	1.5	20	15	US-10-390-045-9	Sequence 9, Appli
	18	20	1.5	20	17	US-10-434-479-9	Sequence 9, Appli
	19	20	1.5	50	15	US-10-195-072-13	Sequence 13, Appl
	20	20	1.5	50	15	US-10-195-071-13	Sequence 13, Appl
c	21	19	1.4	25	17	US-10-434-479-72	Sequence 72, Appl
c	22	19	1.4	26	13	US-10-236-392-385	Sequence 385, App
	23	19	1.4	28	15	US-10-170-663-6	Sequence 6, Appli
c	24	19	1.4	48	15	US-10-205-942-9	Sequence 9, Appli
	25	19	1.4	48	15	US-10-205-942-10	Sequence 10, Appl
	26	18	1.4	18	10	US-09-500-700-68	Sequence 68, Appl
	27	18	1.4	18	15	US-10-314-405-45	Sequence 45, Appl
c	28	18	1.4	18	17	US-10-627-473-45	Sequence 45, Appl
c	29	18	1.4	20	10	US-09-888-326-410	Sequence 410, App
c	30	18	1.4	20	10	US-09-776-479-243	Sequence 243, App
c	31	18	1.4	20	13	US-10-314-578-243	Sequence 243, App
c	32	18	1.4	20	13	US-09-776-479-243	Sequence 243, App
c	33	18	1.4	20	15	US-10-112-653-235	Sequence 235, App
c	34	18	1.4	20	15	US-10-017-995-243	Sequence 243, App
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c	36	18	1.4	27	9	US-09-848-213-18	Sequence 18, Appl
	37	18	1.4	27	9	US-09-848-213-19	Sequence 19, Appl
	38	18	1.4	28	10	US-09-500-700-38	Sequence 38, Appl
c	39	18	1.4	28	15	US-10-422-934-21	Sequence 21, Appl
	40	18	1.4	30	9	US-09-973-145-11	Sequence 11, Appl
	41	18	1.4	30	15	US-10-174-368A-11	Sequence 11, Appl
	42	18	1.4	30	15	US-10-264-127-12	Sequence 12, Appl
	43	18	1.4	30	16	US-10-339-712-12	Sequence 12, Appl
c	44	18	1.4	30	17	US-10-642-763-19	Sequence 19, Appl
c	45	18	1.4	30	17	US-10-642-763-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-195-072-14
; Sequence 14, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-195-072-14

Query Match 1.8%; Score 24; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGGA 79
||||||||||||||||||||||||
Db 23 GGCGGCGGCGGCGGCGGCGGCGGA 46

RESULT 2
US-10-195-071-14
; Sequence 14, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1

; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-195-071-14

Query Match 1.8%; Score 24; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGGA 79
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Db 23 GGCGGCGGCGGCGGCGGCGGCGGA 46

RESULT 3
US-10-434-479-78/c
; Sequence 78, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-434-479-78

Query Match 1.7%; Score 23; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 523 GGAGCTGGAGTTTGTTCAGATCA 545
|||||||||||||||||||||||
Db 23 GGAGCTGGAGTTTGTTCAGATCA 1

RESULT 4
US-10-126-448-2/c
; Sequence 2, Application US/10126448
; Publication No. US20030148422A1
; GENERAL INFORMATION:
; APPLICANT: Doring, Volker
; APPLICANT: Nangle, Leslie A.
; APPLICANT: Hendrickson, Tamara L.
; APPLICANT: de Crecy-Lagard, Valerie
; APPLICANT: Schimmel, Paul
; APPLICANT: Marliere, Philippe
; TITLE OF INVENTION: Method for Diversifying the Chemical
; TITLE OF INVENTION: Composition of Proteins Produced in vivo by Genetically
; TITLE OF INVENTION: Disabling the Editing Function of their Aminoacyl tRNA
; TITLE OF INVENTION: Synthetases
; FILE REFERENCE: CABI-004
; CURRENT APPLICATION NUMBER: US/10/126,448
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/285,495
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: N = phosphorylated cytidine
US-10-126-448-2

Query Match 1.7%; Score 23; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGG 78
|||||||||||||||||||||||
Db 43 GGCGGCGGCGGCGGCGGCGGCGG 21

RESULT 5
US-10-390-045-8/c
; Sequence 8, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-390-045-8

Query Match 1.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 838 CGAGATCGACCTGCCACCCACC 859
||||||||||||||||||||||
Db 22 CGAGATCGACCTGCCACCCACC 1

RESULT 6
US-10-434-479-8/c
; Sequence 8, Application US/10434479
; Publication No. US20040092469A1

; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-434-479-8

Query Match 1.7%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 838 CGAGATCGACCTGCCACCCACC 859
||||||||||||||||||||||
Db 22 CGAGATCGACCTGCCACCCACC 1

RESULT 7
US-10-434-479-70/c
; Sequence 70, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-434-479-70

Query Match 1.7%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1246 GAAGGATAAACAGAAAGGACAC 1267
||||||||||||||||||||||
Db 22 GAAGGATAAACAGAAAGGACAC 1

RESULT 8
US-09-828-034-10/c
; Sequence 10, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-10

Query Match 1.6%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGC 76
|||||||||||||||||||||
Db 21 GGCGGCGGCGGCGGCGGCGGC 1

RESULT 9
US-10-157-382-7/c
; Sequence 7, Application US/10157382
; Publication No. US20030082668A1
; GENERAL INFORMATION:
; APPLICANT: TAMAI, Katsuyuki
; APPLICANT: MIYAZAKI, Toshiaki
; APPLICANT: WADA, Emi
; APPLICANT: TATSUZAWA, Ayumi
; TITLE OF INVENTION: METHOD FOR MEASURING THE ACTIVITY OF DEACETYLASE
; TITLE OF INVENTION: AND METHOD OF SCREENING FOR INHIBITORS AND ACCELERATORS
; TITLE OF INVENTION: OF THE ENZYME
; FILE REFERENCE: M3-109PCT-US(CIP)
; CURRENT APPLICATION NUMBER: US/10/157,382
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: PCT/JP00/08417
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: JP 1999-338565
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
; OTHER INFORMATION: Synthesized Sequence
US-10-157-382-7

Query Match 1.6%; Score 21; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 560 GTGATGATGGTGATGGTGGTG 580
|||||||||||||||||||||
Db 35 GTGATGATGGTGATGGTGGTG 15

RESULT 10
US-10-157-382-8
; Sequence 8, Application US/10157382
; Publication No. US20030082668A1
; GENERAL INFORMATION:
; APPLICANT: TAMAI, Katsuyuki
; APPLICANT: MIYAZAKI, Toshiaki
; APPLICANT: WADA, Emi
; APPLICANT: TATSUZAWA, Ayumi
; TITLE OF INVENTION: METHOD FOR MEASURING THE ACTIVITY OF DEACETYLASE
; TITLE OF INVENTION: AND METHOD OF SCREENING FOR INHIBITORS AND ACCELERATORS
; TITLE OF INVENTION: OF THE ENZYME
; FILE REFERENCE: M3-109PCT-US(CIP)
; CURRENT APPLICATION NUMBER: US/10/157,382
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: PCT/JP00/08417
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: JP 1999-338565
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
; OTHER INFORMATION: Synthesized Sequence
US-10-157-382-8

Query Match 1.6%; Score 21; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 560 GTGATGATGGTGATGGTGGTG 580
||||||||||||||||||||||
Db 9 GTGATGATGGTGATGGTGGTG 29

RESULT 11
US-09-888-326-410
; Sequence 410, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 410
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-410

Query Match 1.5%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGG 75
||||||||||||||||||||
Db 1 GGCGGCGGCGGCGGCGGCGG 20

RESULT 12
US-09-776-479-243
; Sequence 243, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-243

Query Match 1.5%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGG 75
||||||||||||||||||||
Db 1 GGCGGCGGCGGCGGCGGCGG 20

RESULT 13
US-10-314-578-243
; Sequence 243, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-243

Query Match 1.5%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGG 75
||||||||||||||||||||
Db 1 GGCGGCGGCGGCGGCGGCGG 20

RESULT 14
US-09-776-479-243
; Sequence 243, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-243

Query Match 1.5%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         56 GGCGGCGGCGGCGGCGGCGG 75
              ||||||||||||||||||||
Db          1 GGCGGCGGCGGCGGCGGCGG 20
```

RESULT 15
US-10-112-653-235
; Sequence 235, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-235

Query Match 1.5%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         56 GGCGGCGGCGGCGGCGGCGG 75
              ||||||||||||||||||||
Db          1 GGCGGCGGCGGCGGCGGCGG 20
```

Search completed: July 1, 2004, 23:29:54
Job time : 648 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 19:03:10 ; Search time 3776 Seconds
(without alignments)
10447.018 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcggtctcggagcga.....ctgcgtaggtgaaaaggcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	1.7	33	10	BE886705	BE886705 601507961
	2	22	1.7	24	14	CF291636	CF291636 14ROOT--0
	3	22	1.7	50	9	AU107980	AU107980 AU107980
	4	20	1.5	35	2	HSM009944	A1045094 Homo sapi
	5	20	1.5	39	10	BE871689	BE871689 601449550
	6	20	1.5	48	29	CG779308	CG779308 1123033B1
c	7	19	1.4	39	10	BE871689	BE871689 601449550
c	8	18	1.4	24	14	CF291636	CF291636 14ROOT--0
c	9	18	1.4	33	10	BE886705	BE886705 601507961
	10	18	1.4	34	28	AZ761910	AZ761910 1M0556C05
	11	18	1.4	43	28	CC199634	CC199634 XH740 Bay
	12	18	1.4	46	28	AZ993993	AZ993993 2M0279E13
c	13	18	1.4	48	29	CG779308	CG779308 1123033B1
c	14	18	1.4	50	9	AU107980	AU107980 AU107980
	15	17	1.3	27	28	AZ842796	AZ842796 2M0141I20
	16	17	1.3	33	28	AZ401045	AZ401045 1M0167P03
c	17	17	1.3	35	2	HSM009944	A1045094 Homo sapi
c	18	17	1.3	41	28	AZ779226	AZ779226 2M0015B21
c	19	17	1.3	43	28	CC199634	CC199634 XH740 Bay
	20	17	1.3	44	12	BI767274	BI767274 603057978
	21	17	1.3	44	28	AZ635754	AZ635754 1M0493J08
	22	17	1.3	45	12	BI772215	BI772215 603056165
c	23	17	1.3	45	12	BI772215	BI772215 603056165
c	24	17	1.3	49	10	BF970690	BF970690 602273861
	25	17	1.3	50	9	AU104810	AU104810 AU104810
	26	16	1.2	20	14	CF317946	CF317946 HD--07-N0
c	27	16	1.2	20	14	CF317946	CF317946 HD--07-N0
	28	16	1.2	37	14	CF328207	CF328207 NACL--03-
c	29	16	1.2	40	10	BE397229	BE397229 601290723
c	30	16	1.2	41	10	BE264159	BE264159 601191516
c	31	16	1.2	44	12	BI767274	BI767274 603057978
	32	16	1.2	50	9	AU102484	AU102484 AU102484
c	33	16	1.2	50	9	AU102609	AU102609 AU102609
c	34	16	1.2	50	9	AU102610	AU102610 AU102610
	35	16	1.2	50	9	AU103688	AU103688 AU103688
	36	16	1.2	50	9	AU103691	AU103691 AU103691
c	37	16	1.2	50	9	AU104498	AU104498 AU104498
c	38	16	1.2	50	9	AU104499	AU104499 AU104499
c	39	16	1.2	50	9	AU104500	AU104500 AU104500
c	40	16	1.2	50	9	AU104501	AU104501 AU104501
c	41	16	1.2	50	9	AU104502	AU104502 AU104502
	42	16	1.2	50	9	AU104515	AU104515 AU104515
	43	16	1.2	50	9	AU104520	AU104520 AU104520
	44	16	1.2	50	9	AU104811	AU104811 AU104811
c	45	16	1.2	50	9	AU106823	AU106823 AU106823

ALIGNMENTS

RESULT 1
BE886705
LOCUS BE886705 33 bp mRNA linear EST 20-OCT-2000
DEFINITION 601507961F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909591 5', mRNA sequence.
ACCESSION BE886705
VERSION BE886705.1 GI:10341256
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 33)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9723 row: i column: 16
High quality sequence stop: 33.

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FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3909591"
                     /tissue_type="leicmyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
ORIGIN

  Query Match             1.7%;  Score 23;  DB 10;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 GAGGCGGCGGCGGCGGCGGCGGC 76
              |||||||||||||||||||||||
Db         11 GAGGCGGCGGCGGCGGCGGCGGC 33


RESULT 2
CF291636
LOCUS       CF291636                 24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-C09, mRNA sequence.
ACCESSION   CF291636
VERSION     CF291636.1  GI:33660669
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN

  Query Match             1.7%;  Score 22;  DB 14;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCG 77
              ||||||||||||||||||||||
Db          3 GGCGGCGGCGGCGGCGGCGGCG 24
```

```
RESULT 3
AU107980
LOCUS       AU107980                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107980 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV62238, mRNA sequence.
ACCESSION   AU107980
VERSION     AU107980.1  GI:13557502
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ZRV62238"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             1.7%;  Score 22;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 GGCGGCGGCGGCGGCGGCGGAG 80
              ||||||||||||||||||||||
Db         10 GGCGGCGGCGGCGGCGGCGGAG 31


RESULT 4
HSM009944
ID   HSM009944  standard; mRNA; EST; 35 BP.
XX
AC   AL045094;
XX
SV   AL045094.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434L174_r1  (from clone DKFZp434L174)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-35
RA   Wambutt R., Heubner D., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
```

```
XX
CC   Clone from S. Wiemann, sequenced by AGOWA within the cDNA
CC   sequencing consortium of the German Genome Project
CC   s1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .35
FT                   /db_xref="taxon:9606"
FT                   /mol_type="mRNA"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434L174"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; sites NotI + SalI"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 35 BP; 1 A; 12 C; 20 G; 2 T; 0 other;

  Query Match             1.5%;  Score 20;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGAGGCGGCGGCGGCGGCGG 72
              ||||||||||||||||||||
Db          9 GGAGGCGGCGGCGGCGGCGG 28


RESULT 5
BE871689
LOCUS       BE871689                 39 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601449550F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853381 5',
            mRNA sequence.
ACCESSION   BE871689
VERSION     BE871689.1  GI:10320465
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9577  row: c  column: 14
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3853381"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_65"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "
ORIGIN

  Query Match             1.5%;  Score 20;  DB 10;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGG 75
              ||||||||||||||||||||
Db         11 GGCGGCGGCGGCGGCGGCGG 30


RESULT 6
CG779308
LOCUS       CG779308                 48 bp    DNA     linear   GSS 29-OCT-2003
DEFINITION  1123033B10.2EL_x1 1123 - RescueMu Grid L Zea mays genomic, genomic
            survey sequence.
ACCESSION   CG779308
VERSION     CG779308.1  GI:38040097
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1123033  row: 14
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="1123 - RescueMu Grid L"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.' Grid L was grown in Molokai in 2001. DNA was
                     extracted from leaf strips, double digested using BamHI
                     and BglII, and ligated to form circular plasmids. DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."
ORIGIN

  Query Match             1.5%;  Score 20;  DB 29;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         57 GCGGCGGCGGCGGCGGCGGC 76
              ||||||||||||||||||||
Db          8 GCGGCGGCGGCGGCGGCGGC 27


RESULT 7
BE871689/c
LOCUS       BE871689                 39 bp    mRNA    linear   EST 20-OCT-2000
```

```
DEFINITION  601449550F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853381 5',
            mRNA sequence.
ACCESSION   BE871689
VERSION     BE871689.1  GI:10320465
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9577  row: c  column: 14
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3853381"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_65"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.  Library constructed by Life
                     Technologies.  "
ORIGIN

  Query Match             1.4%;  Score 19;  DB 10;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+04;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        440 ACCGCCGCCGCCGCCGCCG 458
              ||||||||||||||||||||
Db         31 ACCGCCGCCGCCGCCGCCG 13


RESULT 8
CF291636/c
LOCUS       CF291636                  24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-C09, mRNA sequence.
ACCESSION   CF291636
VERSION     CF291636.1  GI:33660669
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN

  Query Match             1.4%;  Score 18;  DB 14;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 CCGCCGCCGCCGCCGCCG 458
              ||||||||||||||||||
Db         22 CCGCCGCCGCCGCCGCCG 5


RESULT 9
BE886705/c
LOCUS       BE886705                  33 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601507961F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909591 5',
            mRNA sequence.
ACCESSION   BE886705
VERSION     BE886705.1  GI:10341256
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9723  row: i  column: 16
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3909591"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
ORIGIN

  Query Match             1.4%;  Score 18;  DB 10;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 CCGCCGCCGCCGCCGCCG 458
              ||||||||||||||||||
Db         32 CCGCCGCCGCCGCCGCCG 15
```

```
RESULT 10
AZ761910
LOCUS       AZ761910                34 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0556C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0556C05 R, genomic survey sequence.
ACCESSION   AZ761910
VERSION     AZ761910.1  GI:12871328
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0556  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0556C05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             1.4%;  Score 18;  DB 28;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        554 GTGGTGGTGATGATGGTG 571
              ||||||||||||||||||
Db         14 GTGGTGGTGATGATGGTG 31
```

```
RESULT 11
CC199634
LOCUS       CC199634                43 bp    mRNA    linear   GSS 09-MAY-2003
DEFINITION  XH740 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
            sequence.
ACCESSION   CC199634
VERSION     CC199634.1  GI:30479674
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   BayGenomics.
  TITLE     http://baygenomics.ucsf.edu/
  JOURNAL   Unpublished (2001)
COMMENT     Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CELL_LINE&KEY=XH740
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /clone_lib="BayGenomics Gene Trap Library pGT1Lxf"
                     /note="Vector: pGT1Lxf"
ORIGIN

  Query Match             1.4%;  Score 18;  DB 28;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGC 73
              ||||||||||||||||||
Db         25 GGCGGCGGCGGCGGCGGC 42
```

```
RESULT 12
AZ993993
LOCUS       AZ993993                46 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0279E13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0279E13 F, genomic survey sequence.
ACCESSION   AZ993993
VERSION     AZ993993.1  GI:13865220
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

```
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0279  row: E  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 46.
FEATURES              Location/Qualifiers
     source           1. .46
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0279E13"
                      /sex="Female"
                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC2M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (female) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             1.4%;  Score 18;  DB 28;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        561 TGATGATGGTGATGGTGG 578
              ||||||||||||||||||
Db         29 TGATGATGGTGATGGTGG 46


RESULT 13
CG779308/c
LOCUS       CG779308                 48 bp    DNA     linear   GSS 29-OCT-2003
DEFINITION  1123033B10.2EL_x1 1123 - RescueMu Grid L Zea mays genomic, genomic
            survey sequence.
ACCESSION   CG779308
VERSION     CG779308.1  GI:38040097
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1123033  row: 14
            Class: transposon-tagged.
FEATURES              Location/Qualifiers
     source           1. .48
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /cultivar="mixed background W23/A188/B73/K55"
                      /db_xref="taxon:4577"
                      /tissue_type="leaf"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="1123 - RescueMu Grid L"
                      /note="Organ: leaf; Vector: RescueMu (engineered from
                      pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                      RescueMu is a 4.9 kb, modified maize Mu transposon
                      designed to allow plasmid rescue from total genomic DNA.
                      Mu elements insert preferentially into transcription
                      units. For more information on RescueMu, go to the web
                      site 'www.zmdb.iastate.edu' and follow the links for
                      'RescueMu.' Grid L was grown in Molokai in 2001. DNA was
                      extracted from leaf strips, double digested using BamHI
                      and BglII, and ligated to form circular plasmids. DH10B
                      cells were transformed and then screened on LB plates with
                      ampicillin."
ORIGIN

  Query Match             1.4%;  Score 18;  DB 29;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 CCGCCGCCGCCGCCGCCG 458
              ||||||||||||||||||
Db         26 CCGCCGCCGCCGCCGCCG 9


RESULT 14
AU107980/c
LOCUS       AU107980                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107980 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV62238, mRNA sequence.
ACCESSION   AU107980
VERSION     AU107980.1  GI:13557502
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES              Location/Qualifiers
     source           1. .50
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="ZRV62238"
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/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

Query Match 1.4%; Score 18; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 CCGCCGCCGCCGCCGCCG 458
||||||||||||||||||
Db 29 CCGCCGCCGCCGCCGCCG 12

RESULT 15
AZ842796
LOCUS AZ842796 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0141I20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0141I20 F, genomic survey sequence.
ACCESSION AZ842796
VERSION AZ842796.1 GI:13012704
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0141 row: I column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES Location/Qualifiers
source 1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0141I20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 1.3%; Score 17; DB 28; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.7e+04;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 567 TGGTGATGGTGGTGGTG 583
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Db 11 TGGTGATGGTGGTGGTG 27

Search completed: July 1, 2004, 21:51:07
Job time : 3778 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 19:04:19 ; Search time 115 Seconds
(without alignments)
6374.697 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcggtctcggagcga.....ctgcgtaggtgaaaaggcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	1.8	30	4	US-09-475-947A-332	Sequence 332, App
	2	24	1.8	50	4	US-09-930-181-14	Sequence 14, Appl
	3	23	1.7	25	1	US-08-374-144-3	Sequence 3, Appli
	4	23	1.7	25	1	US-08-775-164-3	Sequence 3, Appli
	5	23	1.7	25	2	US-08-775-609-3	Sequence 3, Appli
	6	23	1.7	25	2	US-08-775-607-3	Sequence 3, Appli
	7	23	1.7	25	5	PCT-US93-06828-3	Sequence 3, Appli
c	8	23	1.7	30	1	US-08-068-747-2	Sequence 2, Appli
	9	23	1.7	33	1	US-08-068-747-7	Sequence 7, Appli
c	10	23	1.7	45	4	US-09-497-933A-22	Sequence 22, Appl
	11	23	1.7	48	4	US-09-497-933A-19	Sequence 19, Appl
c	12	22	1.7	22	4	US-09-769-482-8	Sequence 8, Appli
c	13	21	1.6	21	2	US-08-863-639A-52	Sequence 52, Appl
c	14	21	1.6	21	2	US-08-863-639A-55	Sequence 55, Appl
	15	21	1.6	21	2	US-08-863-639A-56	Sequence 56, Appl
c	16	21	1.6	21	2	US-08-863-639A-67	Sequence 67, Appl
	17	21	1.6	21	2	US-08-863-639A-68	Sequence 68, Appl
	18	21	1.6	21	2	US-08-863-639A-71	Sequence 71, Appl
	19	21	1.6	21	2	US-08-416-214A-11	Sequence 11, Appl
	20	20	1.5	20	3	US-09-030-701-65	Sequence 65, Appl
	21	20	1.5	20	4	US-09-082-649B-57	Sequence 57, Appl
	22	20	1.5	20	4	US-09-769-482-9	Sequence 9, Appli
c	23	20	1.5	24	2	US-08-570-155-16	Sequence 16, Appl
	24	20	1.5	24	2	US-08-570-155-17	Sequence 17, Appl
c	25	20	1.5	50	3	US-08-753-247-22	Sequence 22, Appl
	26	20	1.5	50	4	US-09-930-181-13	Sequence 13, Appl
	27	19	1.4	28	3	US-09-025-580-6	Sequence 6, Appli
c	28	19	1.4	48	4	US-09-438-268-9	Sequence 9, Appli
	29	19	1.4	48	4	US-09-438-268-10	Sequence 10, Appl
c	30	19	1.4	49	1	US-08-155-171B-27	Sequence 27, Appl
	31	19	1.4	49	1	US-08-155-171B-28	Sequence 28, Appl
c	32	19	1.4	49	2	US-08-435-998-27	Sequence 27, Appl
	33	19	1.4	49	2	US-08-435-998-28	Sequence 28, Appl
	34	19	1.4	49	4	US-09-813-781-69	Sequence 69, Appl
c	35	18	1.4	20	3	US-09-030-701-65	Sequence 65, Appl
c	36	18	1.4	20	4	US-09-082-649B-57	Sequence 57, Appl
	37	18	1.4	21	2	US-08-863-639A-52	Sequence 52, Appl
	38	18	1.4	21	2	US-08-863-639A-55	Sequence 55, Appl
c	39	18	1.4	21	2	US-08-863-639A-56	Sequence 56, Appl
	40	18	1.4	21	2	US-08-863-639A-67	Sequence 67, Appl
c	41	18	1.4	21	2	US-08-863-639A-68	Sequence 68, Appl
c	42	18	1.4	21	2	US-08-863-639A-71	Sequence 71, Appl
c	43	18	1.4	21	2	US-08-416-214A-11	Sequence 11, Appl
	44	18	1.4	24	2	US-08-570-155-16	Sequence 16, Appl
c	45	18	1.4	24	2	US-08-570-155-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-475-947A-332
; Sequence 332, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-332

Query Match 1.8%; Score 24; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         56 GGCGGCGGCGGCGGCGGCGGCGGA 79
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Db          7 GGCGGCGGCGGCGGCGGCGGCGGA 30
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RESULT 2
US-09-930-181-14
; Sequence 14, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-181-14

Query Match 1.8%; Score 24; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          56 GGCGGCGGCGGCGGCGGCGGCGGA 79
               ||||||||||||||||||||||||
Db          23 GGCGGCGGCGGCGGCGGCGGCGGA 46


RESULT 3
US-08-374-144-3
; Sequence 3, Application US/08374144
; Patent No. 5629147
;  GENERAL INFORMATION:
;    APPLICANT:  Aprogenex, Inc.
;    TITLE OF INVENTION:  Enriching and Identifying Fetal Cells
;    TITLE OF INVENTION:  Maternal Blood For In Situ Hybridization
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Elman Wilf & Fried
;      STREET:  20 West Third Street, P.O. Box 703
;      CITY:  Media
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19063-8969
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 720K diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,144
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gerry J. Elman
;      REGISTRATION NUMBER:  24,404
;      REFERENCE/DOCKET NUMBER:  M19-085
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-892-9580
;      TELEFAX:  610-892-9577
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-374-144-3

  Query Match             1.7%;  Score 23;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          56 GGCGGCGGCGGCGGCGGCGGCGG 78
               |||||||||||||||||||||||
Db           2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 4
US-08-775-164-3
; Sequence 3, Application US/08775164
; Patent No. 5766843
;  GENERAL INFORMATION:
;    APPLICANT:  Aprogenex, Inc.
;    TITLE OF INVENTION:  Enriching and Identifying Fetal Cells
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Elman & Associates
;      STREET:  20 West Third Street, P.O. Box 1969
;      CITY:  Media
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19063-8969
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 720K diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/775,164
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gerry J. Elman
;      REGISTRATION NUMBER:  24,404
;      REFERENCE/DOCKET NUMBER:  M19-103
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-892-9580
;      TELEFAX:  610-892-9577
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-775-164-3

  Query Match             1.7%;  Score 23;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          56 GGCGGCGGCGGCGGCGGCGGCGG 78
               |||||||||||||||||||||||
Db           2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 5
US-08-775-609-3
; Sequence 3, Application US/08775609
; Patent No. 5858649
;  GENERAL INFORMATION:
;    APPLICANT:  Aprogenex, Inc.
;    TITLE OF INVENTION:  Enriching and Identifying Fetal Cells
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Elman & Associates
;      STREET:  20 West Third Street, P.O. Box 1969
;      CITY:  Media
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19063-8969
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 720K diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/775,609
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gerry J. Elman
;      REGISTRATION NUMBER:  24,404
;      REFERENCE/DOCKET NUMBER:  M19-103
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-892-9580
;      TELEFAX:  610-892-9577
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

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;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-775-609-3

  Query Match             1.7%;  Score 23;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 6
US-08-775-607-3
; Sequence 3, Application US/08775607
; Patent No. 5861253
;  GENERAL INFORMATION:
;    APPLICANT:  Aprogenex, Inc.
;    TITLE OF INVENTION:  Enriching and Identifying Fetal Cells
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Elman & Associates
;      STREET:  20 West Third Street, P.O. Box 1969
;      CITY:  Media
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19063-8969
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 720K diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/775,607
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gerry J. Elman
;      REGISTRATION NUMBER:  24,404
;      REFERENCE/DOCKET NUMBER:  M19-103
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-892-9580
;      TELEFAX:  610-892-9577
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-775-607-3

  Query Match             1.7%;  Score 23;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 7
PCT-US93-06828-3
; Sequence 3, Application PC/TUS9306828
;  GENERAL INFORMATION:
;    APPLICANT:  Asgari, Morteza
;    APPLICANT:  Bresser, Joel
;    APPLICANT:  Cubbage, Michael L
;    APPLICANT:  Prashad, Nagindra
;    TITLE OF INVENTION:  Enriching and Identifying Fetal Cells In Maternal Blood For
;    TITLE OF INVENTION:  In Situ Hybridization
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:
;      STREET:
;      CITY:
;      STATE:
;      COUNTRY:
;      ZIP:
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 Floppy disk - 720 k
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06828
;      FILING DATE:  19930719
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US93-06828-3

  Query Match             1.7%;  Score 23;  DB 5;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 8
US-08-068-747-2/c
; Sequence 2, Application US/08068747
; Patent No. 5695933
;  GENERAL INFORMATION:
;    APPLICANT:  Schalling, Martin
;    APPLICANT:  Hudson, Thomas J.
;    APPLICANT:  Housman, David E.
;    TITLE OF INVENTION:  Direct Determination of Expanded
;    TITLE OF INVENTION:  Nucleotide Repeats in the Human Genome
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusett
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,747
;      FILING DATE:  28-MAY-1993
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  MIT-6141
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic"
US-08-068-747-2

  Query Match           1.7%;  Score 23;  DB 1;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 1.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db         29 GGCGGCGGCGGCGGCGGCGGCGG 7


RESULT 9
US-08-068-747-7
; Sequence 7, Application US/08068747
; Patent No. 5695933
;  GENERAL INFORMATION:
;    APPLICANT:  Schalling, Martin
;    APPLICANT:  Hudson, Thomas J.
;    APPLICANT:  Housman, David E.
;    TITLE OF INVENTION:  Direct Determination of Expanded
;    TITLE OF INVENTION:  Nucleotide Repeats in the Human Genome
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusett
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,747
;      FILING DATE:  28-MAY-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  MIT-6141
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic"
US-08-068-747-7

  Query Match           1.7%;  Score 23;  DB 1;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db          2 GGCGGCGGCGGCGGCGGCGGCGG 24


RESULT 10
US-09-497-933A-22/c
; Sequence 22, Application US/09497933A
; Patent No. 6329147
; GENERAL INFORMATION:
;  APPLICANT:  Wagner, Robert Jr. E.
;  TITLE OF INVENTION:  METHODS FOR DETECTION OF A TRIPLET REPEAT BLOCK AND A
;  TITLE OF INVENTION:  FUNCTIONAL MISMATCH BINDING PROTEIN IN A BIOLOGICAL
;  TITLE OF INVENTION:  FLUID SAMPLE
;  FILE REFERENCE:  9408-044
;  CURRENT APPLICATION NUMBER: US/09/497,933A
;  CURRENT FILING DATE:  2000-02-04
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 22
;    LENGTH: 45
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Probe
;    NAME/KEY: modified_base
;    LOCATION: (1)..(9)
;    OTHER INFORMATION: n = a, c, g or t
;    NAME/KEY: modified_base
;    LOCATION: (37)..(45)
;    OTHER INFORMATION: n = a, c, g or t
US-09-497-933A-22

  Query Match           1.7%;  Score 23;  DB 4;  Length 45;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 GGCGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||||
Db         35 GGCGGCGGCGGCGGCGGCGGCGG 13


RESULT 11
US-09-497-933A-19
; Sequence 19, Application US/09497933A
; Patent No. 6329147
; GENERAL INFORMATION:
;  APPLICANT:  Wagner, Robert Jr. E.
;  TITLE OF INVENTION:  METHODS FOR DETECTION OF A TRIPLET REPEAT BLOCK AND A
;  TITLE OF INVENTION:  FUNCTIONAL MISMATCH BINDING PROTEIN IN A BIOLOGICAL
;  TITLE OF INVENTION:  FLUID SAMPLE
;  FILE REFERENCE:  9408-044
;  CURRENT APPLICATION NUMBER: US/09/497,933A
;  CURRENT FILING DATE:  2000-02-04
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 19
;    LENGTH: 48
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Probe
;    NAME/KEY: modified_base
;    LOCATION: (1)..(9)
;    OTHER INFORMATION: n = a, c, g or t
;    NAME/KEY: modified_base
;    LOCATION: (40)..(48)
;    OTHER INFORMATION: n = a, c, g or t
US-09-497-933A-19

  Query Match           1.7%;  Score 23;  DB 4;  Length 48;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
```

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  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          56 GGCGGCGGCGGCGGCGGCGGCGG 78
               |||||||||||||||||||||||
Db          11 GGCGGCGGCGGCGGCGGCGGCGG 33


RESULT 12
US-09-769-482-8/c
; Sequence 8, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
;  APPLICANT: SRIVASTAVA, SHIV
;  APPLICANT:  MOUL, JUDD W.
;  APPLICANT:  XU, LINDA L.
;  APPLICANT:  SEGAWA, TAKEHIKO
;  TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
;  TITLE OF INVENTION:  POYNUCLEOTIDE ARRAY
;  FILE REFERENCE: 04995.0057-00000
;  CURRENT APPLICATION NUMBER: US/09/769,482
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 60/178,772
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: 60/179,045
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-769-482-8

  Query Match             1.7%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         838 CGAGATCGACCTGCCACCCACC 859
               ||||||||||||||||||||||
Db          22 CGAGATCGACCTGCCACCCACC 1


RESULT 13
US-08-863-639A-52/c
; Sequence 52, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-52

  Query Match             1.6%;  Score 21;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          58 CGGCGGCGGCGGCGGCGGCGG 78
               |||||||||||||||||||||
Db          21 CGGCGGCGGCGGCGGCGGCGG 1


RESULT 14
US-08-863-639A-55/c
; Sequence 55, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-55

  Query Match             1.6%;  Score 21;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          57 GCGGCGGCGGCGGCGGCGGCG 77
               |||||||||||||||||||||
Db          21 GCGGCGGCGGCGGCGGCGGCG 1
```

```
RESULT 15
US-08-863-639A-56
; Sequence 56, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-56

  Query Match             1.6%;  Score 21;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CGGCGGCGGCGGCGGCGGCGG 78
              |||||||||||||||||||||
Db          1 CGGCGGCGGCGGCGGCGGCGG 21


Search completed: July  1, 2004, 21:53:07
Job time : 115 secs
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